

## SEQUENCE LISTING

<110> MIETKIEWSKA, Elzbieta et al.

<120> FATTY ACID ELONGASE (FAE) GENES AND THEIR UTILITY IN INCREASING ERUCIC ACID AND OTHER VERY LONG-CHAIN FATTY ACID PROPORTIONS IN SEED OIL

<130> PAT 989W-2

<140> US 10/596,024

<141> 2004-11-24

<150> US 60/524,645

<151> 2003-11-25

<160> 27

<170> PatentIn version 3.2

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<211> 18

<212> DNA

<213> Artificial

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<223> F1 Forward Primer

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<213> Artificial

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Leu Gly Gly Met Gly Cys

1 5

<210> 3

<211> 18

<212> DNA

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<223> R1 Reverse Primer

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trtaygcyan ctcrtacc 18

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<223> F3 Forward Primer

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<212> DNA

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<223> R3 Reverse Primer

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<212> DNA

<213> Artificial

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<223> R6 Reverse Primer

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21

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&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; F6 Forward Primer

&lt;400&gt; 16

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&lt;210&gt; 17

&lt;211&gt; 27

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&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; R7 Reverse Primer

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&lt;211&gt; 22

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<220>

<223> OM087 Primer

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<223> OM088 Primer

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33

<210> 22

<211> 503

<212> PRT

<213> Tropaeolum majus

&lt;400&gt; 22

Met Ser Gly Thr Lys Ala Thr Ser Val Ser Val Pro Leu Pro Asp Phe  
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Lys Gln Ser Val Asn Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Ser  
20 25 30

Ile Thr His Ala Met Tyr Leu Phe Leu Thr Pro Leu Leu Ile Met  
35 40 45

Ser Ala Gln Ile Ser Thr Phe Ser Ile Gln Asp Phe His His Leu Tyr  
50 55 60

Asn His Leu Ile Leu His Asn Leu Ser Ser Leu Ile Leu Cys Ile Ala  
65 70 75 80

Leu Leu Leu Phe Val Leu Thr Leu Tyr Phe Leu Thr Arg Pro Thr Pro  
85 90 95

Val Tyr Leu Leu Asn Phe Ser Cys Tyr Lys Pro Asp Ala Ile His Lys  
100 105 110

Cys Asp Arg Arg Arg Phe Met Asp Thr Ile Arg Gly Met Gly Thr Tyr  
115 120 125

Thr Glu Glu Asn Ile Glu Phe Gln Arg Lys Val Leu Glu Arg Ser Gly  
130 135 140

Ile Gly Glu Ser Ser Tyr Leu Pro Pro Thr Val Phe Lys Ile Pro Pro  
145 150 155 160

Arg Val Tyr Asp Ala Glu Glu Arg Ala Glu Ala Glu Met Leu Met Phe  
165 170 175

Gly Ala Val Asp Gly Leu Phe Glu Lys Ile Ser Val Lys Pro Asn Gln  
180 185 190

Ile Gly Val Leu Val Val Asn Cys Gly Leu Phe Asn Pro Ile Pro Ser  
195 200 205

Leu Ser Ser Met Ile Val Asn Arg Tyr Lys Met Arg Gly Asn Val Phe  
210 215 220

Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Val Ile Ser Ile  
225 230 235 240

Asp Leu Ala Lys Asp Leu Leu Gln Val Arg Pro Asn Ser Tyr Ala Leu  
245 250 255

Val Val Ser Leu Glu Cys Ile Ser Lys Asn Leu Tyr Leu Gly Glu Gln  
260 265 270

Arg Ser Met Leu Val Ser Asn Cys Leu Phe Arg Met Gly Gly Ala Ala  
275 280 285

Ile Leu Leu Ser Asn Lys Met Ser Asp Arg Trp Arg Ser Lys Tyr Arg  
290 295 300

Leu Val His Thr Val Arg Thr His Lys Gly Thr Glu Asp Asn Cys Phe  
305 310 315 320

Ser Cys Val Thr Arg Lys Glu Asp Ser Asp Gly Lys Ile Gly Ile Ser  
325 330 335

Leu Ser Lys Asn Leu Met Ala Val Ala Gly Asp Ala Leu Lys Thr Asn  
340 345 350

Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu  
355 360 365

Phe Phe Ala Thr Leu Val Gly Lys Lys Val Phe Lys Met Lys Leu Gln  
370 375 380

Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys Ile His  
385 390 395 400

Ala Gly Gly Arg Ala Val Leu Asp Glu Leu Glu Lys Asn Leu Lys Leu  
405 410 415

Ser Ser Trp His Met Glu Pro Ser Arg Met Ser Leu Tyr Arg Phe Gly  
420 425 430

Asn Thr Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ser Glu Ala  
435 440 445

Lys Gly Arg Ile Lys Lys Gly Asp Arg Val Trp Gln Ile Ala Phe Gly  
450 455 460

Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg Asn Val  
465 470 475 480

Asn Pro Ala Glu Glu Lys Asn Pro Trp Met Asp Glu Ile His Leu Phe  
485 490 495

Pro Val Glu Val Pro Leu Asn  
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<210> 23  
<211> 1765  
<212> DNA  
<213> Tropaeolum majus

<400> 23

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tcactcatgc aatgtatctt ttcttaaccc ctcttcttct cataatgtct gctcaaatct 180

caactttctc tattcaagat ttccaccatc ttataacca tcttacccctc cacaatctct 240

catcccttat cctatgcattc gctctccctc tcttcgtctt aaccctctat ttccctactc 300

gtcccacgcc tgtttattta ctcaacttctt ctgttacaa accggatgct attcacaat 360

gcgaccggcc tcgttcatg gacaccattc gtggaatggg tacttatacg gaagagaaca 420

tcgagttca aaggaaagtctt ctagaaaggtt ccggaaatagg ggaatcgtct tatcttctc 480

cgactgtgtt taaaattcctt cctagggttt acgatgcgga ggaacgcgcg gaggctgaga 540

tgctgatgtt cggtgcgggtt gatgggttt tcgagaaaat atctgttaaa ccgaatcaaa 600

tcggggttt ggttgtaat tgtgggttgtt ttaatccgat accgtctta tctccatga 660

ttgtgaatcg ctacaagatg agagggaatg ttttagtta taattgggt ggaatgggt 720  
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aaaaaaaaaaaa aaaaaaaaaaaa aaaaa 1765

<210> 24  
<211> 506  
<212> PRT  
<213> Crambe abyssinica

&lt;400&gt; 24

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Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys  
20 25 30

Ala Ser Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr  
35 40 45

Leu Gln His Asn Val Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val  
50 55 60

Phe Gly Ser Ile Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu  
65 70 75 80

Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr Gln Cys Arg Ser Ser Ile  
85 90 95

Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Phe  
100 105 110

Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys  
115 120 125

Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly  
130 135 140

Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu  
145 150 155 160

Thr Glu Gln Val Ile Val Gly Ala Leu Lys Asn Leu Phe Glu Asn Thr  
165 170 175

Lys Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met  
180 185 190

Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys  
195 200 205

Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser

210 215

220

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His  
225 230 235 240

Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn  
245 250 255

Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe  
260 265 270

Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg Asp Arg  
275 280 285

Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly  
290 295 300

Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn  
305 310 315 320

Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Glu Val Ala Gly  
325 330 335

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro  
340 345 350

Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Ala Lys Lys Leu  
355 360 365

Phe Lys Asp Lys Val Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
370 375 380

Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val  
385 390 395 400

Leu Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala Ser Arg  
405 410 415

Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr  
420 425 430

Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
435 440 445

Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
450 455 460

Trp Val Ala Leu Ser Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
465 470 475 480

His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Ala Lys  
485 490 495

Ser Glu Thr Arg Ala Gln Asn Gly Arg Ser  
500 505

<210> 25

<211> 1521

<212> DNA

<213> Crambe abyssinica

<400> 25

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cttcaccact tatattatttc ctatctccaa cacaacgtca taaccatagc tccactctt 180

gccttaccg tttcggttc gattctctac atcgtgaccc ggcccaaacc ggtttacctc 240

gttgagtact catgtcacct tccaccaacg cagtgttagat caagtatctc caaggtcatg 300

gatatatttt atcaagtaag aaaagctgat cctttcgta acgggacatg cgatgactcg 360

tcctggcttg acttcttgag gaagattcaa gaacgttcag gtctaggcga cgaaactcac 420

ggccccgagg gactgcttca ggtccctccc cggaagactt ttgcggcggc gcgtgaagag 480

acggagcaag taatcgctgg tgcgctgaaa aatctattcg agaacaccaa agttaaccct 540

aaagatatacg gtatacttgt ggtgaactca agcatgttta atccaaactcc ttcactctca 600

gcgtggctcg ttaatacttt caagctccga agtaacgtaa gaagcttaa cttggcggc 660

atgggttgc tatagccatt gatctggcta aggacttgtt gcatgtccat 720  
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ctagagaaga atttaggcct agcaccgatc gatgttagagg catcaagatc aacgttacat 1260  
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aacagtgcgg ttgggttagc tttaagcaat gtcaaggctt cgacaaatag tcctggaa 1440  
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<211> 506  
<212> PRT  
<213> Arabidopsis sp.

<400> 26

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			5			10			15						

Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20			25			30						

Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu  
35 40 45

Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe  
50 55 60

Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val  
65 70 75 80

Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser  
85 90 95

Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser  
100 105 110

Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys  
115 120 125

Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly  
130 135 140

Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu  
145 150 155 160

Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr  
165 170 175

Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met  
180 185 190

Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys  
195 200 205

Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser  
210 215 220

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His  
225 230 235 240

Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly  
245 250 255

Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe  
260 265 270

Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg  
275 280 285

Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly  
290 295 300

Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser  
305 310 315 320

Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly  
325 330 335

Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro  
340 345 350

Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu  
355 360 365

Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
370 375 380

Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu  
385 390 395 400

Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg  
405 410 415

Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr  
420 425 430

Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
435 440 445

Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
450 455 460

Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln  
465 470 475 480

His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys

485 490 495

Ser Lys Thr His Val Gln Asn Gly Arg Ser

500 505

&lt;210&gt; 27

&lt;211&gt; 1521

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis sp.

&lt;400&gt; 27

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ctccacaact tccttccta tctccaacac aaccttataa cagtaacttt actctttgc 180

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attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg tgatgatccg 360

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acagagaagg ttatcatcgg tgcgctcgaa aatctattcg agaacaccaa agttaaccct 540

agagagattg gtatacttgtt ggtgaactca agcatgttta atccaactcc ttgcgtatcc 600

gctatggtcg ttaatactttt caagctccga agcaacatca aaagctttaa tctaggagga 660

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aaaaacactt atgctcttgtt ggtgagcact gagaacatca cacaaggcat ttatgctgg 780

gaaaatagat caatgatggtagcaattgc ttgttcgtt ttgggggc cgcgatgg 840

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